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#13
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/817,538

DATE: 10/09/2001

TIME: 08:58:39

Input Set : A:\106101-144.ST25.txt

Output Set: N:\CRF3\10092001\I817538.raw

4 <110> APPLICANT: Li, Zuomei
5 Bonfils, Claire
6 Besterman, Jeffrey
8 <120> TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone
9 Deacetylase Isoforms
11 <130> FILE REFERENCE: 106101.144
13 <140> CURRENT APPLICATION NUMBER: US 09/817,538
14 <141> CURRENT FILING DATE: 2001-03-26
16 <150> PRIOR APPLICATION NUMBER: US 60/192,157
17 <151> PRIOR FILING DATE: 2000-03-24
19 <160> NUMBER OF SEQ ID NOS: 33
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 481
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39 35 40 45
42 Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met
43 50 55 60
46 Thr Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg
47 65 70 75 80
50 Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val
51 85 90 95
54 Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu
55 100 105 110
58 Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln
59 115 120 125
62 Thr Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys
63 130 135 140
66 Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile
67 145 150 155 160
70 Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp
71 165 170 175
74 Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg
75 180 185 190
78 Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr
79 195 200 205
82 Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val
83 210 215 220
86 Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile Phe
87 225 230 235 240

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95          260          265          270
98 Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val Lys
99          275          280          285
102 Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Gly Tyr Thr Ile
103          290          295          300
106 Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr Ala Val Ala Leu Asp
107 305          310          315          320
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126 Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp Pro
127 385          390          395          400
130 Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys Glu
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134 Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys Asn
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191 actccctatc tggggatcgg ttaggttgct tcaatctatc tatcaaagga cagccaagt      960
193 gtgtggaatt tgtcaagagc tttaacctgc ctatgctgat gctgggaggc ggtgggtaca    1020
195 ccattcgtaa cgttgcccgg tgctggacat atgagacagc tgtggccctg gatacggaga    1080
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233 35 40 45
236 Gly Leu Tyr Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Thr Ala
237 50 55 60
240 Glu Glu Met Thr Lys Tyr His Ser Asp Glu Tyr Ile Lys Phe Leu Arg
241 65 70 75 80
244 Ser Ile Arg Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met His Ile
245 85 90 95
248 Pro Phe Asn Val Gly Glu Asp Cys Pro Ala Phe Asp Gly Leu Phe Glu
249 100 105 110
252 Phe Cys Gln Leu Ser Thr Gly Gly Ser Val Ala Gly Ala Val Lys Leu
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256 Asn Arg Gln Gln Thr Asp Met Ala Val Asn Trp Ala Gly Gly Leu His
257 130 135 140
260 His Ala Lys Lys Tyr Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile
261 145 150 155 160
264 Val Leu Ala Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr
265 165 170 175
268 Ile Asp Ile Asp Ile His His Arg Gly Asp Gly Val Glu Glu Ala Phe
269 180 185 190
272 Tyr Thr Thr Asp Arg Val Met Thr Val Ser Phe Tyr Gly Glu Tyr Phe
273 195 200 205
276 Pro Gly Thr Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr
277 210 215 220
280 Tyr Ala Val Asn Phe Pro Met Cys Asp Gly Ile Asp Asp Glu Ser Tyr
281 225 230 235 240

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284 Gly Gln Ile Phe Lys Pro Ile Ile Ser Lys Val Met Glu Met Tyr Gln
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288 Pro Ser Ala Val Val Leu Gln Cys Gly Ala Asp Ser Leu Ser Gly Asp
289                260                265                270
292 Arg Leu Gly Cys Phe Asn Leu Thr Val Lys Gly His Ala Lys Cys Val
293                275                280                285
296 Glu Val Val Lys Thr Phe Asn Leu Pro Leu Leu Met Leu Gly Gly Gly
297                290                295                300
300 Gly Tyr Thr Ile Leu Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr
301 305                310                315                320
304 Ala Val Ala Leu Asp Cys Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp
305                325                330                335
308 Tyr Phe Glu Tyr Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser
309                340                345                350
312 Asn Met Thr Asn Gln Asn Thr Pro Glu Tyr Met Glu Lys Ile Lys Gln
313                355                360                365
316 Arg Leu Phe Glu Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln
317                370                375                380
320 Met Gln Ala Ile Pro Glu Asp Ala Val His Glu Asp Ser Gly Asp Glu
321 385                390                395                400
324 Asp Gly Glu Asp Pro Asp Lys Arg Ile Ser Ile Arg Ala Ser Asp Lys
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328 Arg Ile Ala Cys Asp Glu Glu Phe Ser Asp Ser Glu Asp Glu Gly Glu
329                420                425                430
332 Gly Gly Arg Asn Val Ala Asp His Lys Lys Gly Ala Lys Ala Arg Ile
333                435                440                445
336 Glu Glu Asp Lys Lys Glu Thr Glu Asp Lys Lys Thr Asp Val Lys Glu
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363 tgctactact acgacggtga tattggaaat tattattatg gacagggtca tcccatgaag    300
365 cctcatagaa tccgcatgac ccataacttg ctgttaaatt atggcttaca cagaaaaatg    360
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371 catatattta atgttgagga agattgtcca gcgtttgatg gactctttga gttttgtcag    540
373 ctctcaactg gcggttcagt tgctggagct gtgaagttaa accgacaaca gactgatatg    600
375 gctgttaatt gggctggagg attacatcat gctaagaaat acgaagcatc aggatcctgt    660
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383 agggatattg gtgctggaaa aggcaaatac tatgctgtca attttccaat gtgtgatggg 900
385 atagacgatg agtcatatgg gcagatatatt aagcctatta tctcaaagggt gatggagatg 960
387 tatcaaccta gtgctgtggg attacagtgt ggtgcagact cattatctgg tgatagactg 1020
389 ggttggtttca atctaacagt caaaggatcat gctaaatgtg tagaagttgt aaaaactttt 1080
391 aacttaccat tactgatgct tggaggagggt ggctacacaa tccgtaatgt tgctcgatgt 1140
393 tggacatatg agactgcagt tgcccttgat tgtgagattc ccaacgagtt gccatataat 1200
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397 aaccagaaca ctccagaata tacggaaaag ataaaacagc gtttgtttga aaatttgccg 1320
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VERIFICATION SUMMARY

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